

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 18:47:00 ; Search time 5614 Seconds
(without alignments)
11570.620 Million cell updates/sec

Title: US-09-625-573-1
Perfect score: 2232
Sequence: 1 GGATTGAACAAAGGACGATT.....TATACTATGTTGATAAAG 2232

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
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- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pin.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2232	100.0	2232	6	AR116074
2	2232	100.0	2232	6	I79542 Sequence 1
3	2232	100.0	2232	9	U03882 Human monoc
4	1254	56.2	5471	9	U0924 Human monoc
5	1152	51.6	143068	6	AX335952 Sequence
6	1152	51.6	143068	9	U95626 Homo sapien
7	1101	49.3	185437	9	AC098613 Homo sapi
8	1068	47.8	1068	11	G07239 human STS W
9	980	43.9	1979	6	AR116075
10	980	43.9	1979	6	I79543 Sequence 3
11	980	43.9	1979	9	U03905 Human monoc
12	941	42.2	1083	6	AX232508 Sequence
13	890	39.9	1083	6	AX232506 Sequence
14	890	39.9	1083	6	D29984 Human mRNA
15	839	37.6	1083	6	AX280849 Sequence
16	839	37.6	1083	6	AX280849 Sequence
17	613	27.5	2900	2	AC087602
18	281	12.6	1651	9	HSMP1REC
19	128	5.7	469	11	G50956
20	120	5.4	1083	9	AF013958
21	77	3.4	949	9	AF161930
22	77	3.4	1019	9	AF161922
23	77	3.4	1019	9	AF161923
24	77	3.4	1019	9	AF161924
25	77	3.4	1019	9	AF161925
26	77	3.4	1019	9	AF161926
27	77	3.4	1019	9	AF161927
28	77	3.4	1019	9	AF161928
29	77	3.4	1019	9	AF161929
30	77	3.4	1019	9	AF161931
31	77	3.4	1019	9	AF161932
32	75	3.4	1019	9	AF161933
33	67	3.0	1059	9	AF177887
34	65	2.9	461	6	AR119945
35	65	2.9	792	6	AX427279
36	65	2.9	1018	9	AF161918
37	65	2.9	1019	9	AF161898
38	65	2.9	1019	9	AF161899
39	65	2.9	1019	9	AF161900
40	65	2.9	1019	9	AF161901
41	65	2.9	1019	9	AF161903
42	65	2.9	1019	9	AF161904
43	65	2.9	1019	9	AF161905
44	65	2.9	1019	9	AF161909
45	65	2.9	1019	9	AF161910

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AR116074	AR116074	Sequence 1 from patent US 6132987.	AR116074	AR116074.1	GI:14096396	Unknown.	Unknown.	1 (bases 1 to 2232)	Charo, I.F. and Coughlin, S.R.	Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)	Patent: US 6132987-A 1 17-OCT-2000;
AR116074	AR116074	Sequence 1 from patent US 6132987.	AR116074	AR116074.1	GI:14096396	Unknown.	Unknown.	1 (bases 1 to 2232)	Charo, I.F. and Coughlin, S.R.	Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)	Patent: US 6132987-A 1 17-OCT-2000;

linear DNA PAT 16-MAY-2001

QY	1561	AGAGTGTGGAAGTGTTGATCTCTGGGCACATTAGCCTATGTGCATCGACCATCTAAGTA	1620
Db	1561	AGAGTGTGGAAGTGTTGATCTCTGGGCACATTAGCCTATGTGCATCGACCATCTAAGTA	1620
QY	1621	ATGATGTCGCTTTCAATCACAGTATACGCTCCATCGTGTCATCTCAGCTGGATCTCCATT	1680
Db	1621	ATGATGTCGCTTTCAATCACAGTATACGCTCCATCGTGTCATCTCAGCTGGATCTCCATT	1680
QY	1681	CCTCAGGCTTGCTGCCAAAAGCCCTTTCTGCTGTTTTCTTTTGTATCATATTGAAGTCATGC	1740
Db	1681	CCTCAGGCTTGCTGCCAAAAGCCCTTTCTGCTGTTTTCTTTTGTATCATATTGAAGTCATGC	1740
QY	1741	GTTTAAATCACATTCGAGTGTTTTCAGTGCTTCGACATGTCCTTGATGCTCATATTTCTTC	1800
Db	1741	GTTTAAATCACATTCGAGTGTTTTCAGTGCTTCGACATGTCCTTGATGCTCATATTTCTTC	1800
QY	1801	CTAATTTGCCAGTGGGAAGCTCTTAATCAAATGGCTTCTTAATCAAAGCTTTTAAACCCT	1860
Db	1801	CTAATTTGCCAGTGGGAAGCTCTTAATCAAATGGCTTCTTAATCAAAGCTTTTAAACCCT	1860
QY	1861	ATTGTTAAGAATGGAAGTGGAGAGCTCCCTGAAGTAAGCAAAGACTTCTCTCTTAGT	1920
Db	1861	ATTGTTAAGAATGGAAGTGGAGAGCTCCCTGAAGTAAGCAAAGACTTCTCTCTTAGT	1920
QY	1921	CGAGCCAAGTTAAGAATGTTCTATGTGTGCCAGTGTGTTCTGATCTGATCGACAAG	1980
Db	1921	CGAGCCAAGTTAAGAATGTTCTATGTGTGCCAGTGTGTTCTGATCTGATCGACAAG	1980
QY	1981	AAACACTGGGCTTCTAGAACACGAGCAACTTGGGAAGTGGGAACTAGACTCCCAAGCTGACTATGCC	2040
Db	1981	AAACACTGGGCTTCTAGAACACGAGCAACTTGGGAAGTGGGAACTAGACTCCCAAGCTGACTATGCC	2040
QY	2041	TCTACTTTCAGGCCACATGGCTTAAGAAGTTCAGAAAGAGTGGGACAGACGACAGAAC	2100
Db	2041	TCTACTTTCAGGCCACATGGCTTAAGAAGTTCAGAAAGAGTGGGACAGACGACAGAAC	2100
QY	2101	TTTCACCTTCATATATTGTATGATCCTTAATGAATGCATAAAATGTTAAGTTGATGGTGA	2160
Db	2101	TTTCACCTTCATATATTGTATGATCCTTAATGAATGCATAAAATGTTAAGTTGATGGTGA	2160
QY	2161	TGAATGTAATACTGTTTTTAAACACTATGATTTGAAAAATAATCAATGCTATAACTA	2220
Db	2161	TGAATGTAATACTGTTTTTAAACACTATGATTTGAAAAATAATCAATGCTATAACTA	2220
QY	2221	TGTTGATAAAG 2232	
Db	2221	TGTTGATAAAG 2232	
RESULT 3			
HSU03882		2232 bp mRNA linear PRI 22-JUN-1994	
LOCUS			
DEFINITION		Human monocyte chemoattractant protein 1 receptor (MCP-1RA)	
ACCESSION		alternatively spliced mRNA, complete cds.	
VERSION		U03882	
KEYWORDS		U03882.1 GI:472555	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2232) Charo,I.F., Myers,S.J., Herman,A., Franci,C., Connolly,A.J. and Coughlin,S.R.	
TITLE		Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)	
MEDLINE		94195821	
PUBMED		8146186	
REFERENCE		2 (bases 1 to 2232)	
AUTHORS		Myers,S.J.	
TITLE		Direct Submission	

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BASE COUNT	41194	a	30122	c	32403	g	39349	t	
ORIGIN									
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Best Local Similarity	99.8%; Pred. No. 0;								
Matches 1252; Conservative	0; Mismatches 2; Indels 0; Gaps 0;								
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Db	48253	AGCCTTTTTCACATAGCTCTGGCTGAGGATTCGCCACCTCCCAAAACCAAGTGTGTGA	48312						
QY	1039	GCTCAGGAGTGAGCAGGAGGAAGAATGTGAAGTGTACTACACAAGGACTCCTCGATGGT	1098						
Db	48313	GCTCAGGAGTGAGCAGGAGGAAGAATGTGAAGTGTACTACACAAGGACTCCTCGATGGT	48372						
QY	1099	CGTGAAGAAGAAAGTCAATTTGGCAGAGCCCTGAAGCCAGTCTTCAGGACAAAGAAGGA	1158						
Db	48373	CGTGAAGAAGAAAGTCAATTTGGCAGAGCCCTGAAGCCAGTCTTCAGGACAAAGAAGGA	48432						
QY	1159	GCCTAGACACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCTGGCTTCACAGATG	1218						
Db	48433	GCCTAGACACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCTGGCTTCACAGATG	48492						
QY	1219	TGTGATTCACAGTGTGAATCTTGTGTCTACGTTACGAGGAGGAGGCTGAGAGGAG	1278						
Db	48493	TGTGATTCACAGTGTGAATCTTGTGTCTACGTTACGAGGAGGAGGCTGAGAGGAG	48552						
QY	1279	AGATCCACGCTGGTGTGGAACACATATTTCCAACTACCTTCAGTTCCTCATTTTGT	1338						
Db	48553	AGATCCACGCTGGTGTGGAACACATATTTCCAACTACCTTCAGTTCCTCATTTTGT	48612						
QY	1339	AATACAGGATAGAGTTCAGACTTTTTTAAATAGTAAATTAATAAAGCTGAAAC	1398						
Db	48613	AATACAGGATAGAGTTCAGACTTTTTTAAATAGTAAATTAATAAAGCTGAAAC	48672						
QY	1399	TGCAACTTGAATGTGTAAGAGTATTTGAGTTGCTATCATGCTCAAGCTGAAAT	1458						
Db	48673	TGCAACTTGAATGTGTAAGAGTATTTGAGTTGCTATCATGCTCAAGCTGAAAT	48732						
QY	1459	GCTGATTTAGTCACAGAGATAATTCAGCTTTGAGCTTAAGATTTTGACGAGTGGTAT	1518						
Db	48733	GCTGATTTAGTCACAGAGATAATTCAGCTTTGAGCTTAAGATTTTGACGAGTGGTAT	48792						
QY	1519	GTTTGGGAGACTGCTCAGTCAACCCAAATAGTTGATTTGGCAGGAGTTGGAAGTGTG	1578						
Db	48793	GTTTGGGAGACTGCTCAGTCAACCCAAATAGTTGATTTGGCAGGAGTTGGAAGTGTG	48852						
QY	1579	ATCTGTGGCAGATTTAGCCCTATGTCATGTCAGCATCTAAGTATGATGCTGTTGAATCA	1638						
Db	48853	ATCTGTGGCAGATTTAGCCCTATGTCATGTCAGCATCTAAGTATGATGCTGTTGAATCA	48912						
QY	1639	CAGTATACGCTCCATGCTCTCATCTCAGCTGAGTCCCATTCCTCAGGCTTGCTGCCA	1698						
Db	48913	CAGTATACGCTCCATGCTCTCATCTCAGCTGAGTCCCATTCCTCAGGCTTGCTGCCA	48972						
QY	1699	AAAGCCCTTTGTTGTTTGTATCATTTATGAGTCATGCGCTTAAATCACATTCGAGT	1758						
Db	48973	AAAGCCCTTTGTTGTTTGTATCATTTATGAGTCATGCGCTTAAATCACATTCGAGT	49032						
QY	1759	GTTTCACTGCTCCGACATGCTCTGATGCTCATATTTGTTCCCTTAAATTTGCCAGTGGAA	1818						
Db	49033	GTTTCACTGCTCCGACATGCTCTGATGCTCATATTTGTTCCCTTAAATTTGCCAGTGGAA	49092						
QY	1819	CTCCTAAATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCTATTTGTAAGAATG	1878						
Db	49093	CTCCTAAATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCTATTTGTAAGAATG	49152						
QY	1879	GTGGAAGAGCTCCCTGAAGTAAAGACATTTCTCTTACTGAGCCCAAGTAAAGAATG	1938						
Db	49153	GTGGAAGAGCTCCCTGAAGTAAAGACATTTCTCTTACTGAGCCCAAGTAAAGAATG	49212						
QY	1939	TTCTTATCTTCCCGAGTGTGTTTCTGATCTGATGCAAGCAAGAAACACTGGGCTTCTAGA	1998						

Db 49213 TTCTTATGTTGCCAGTGTGTTCTGATCTGATGTCAGTGCAGCAAGAACACACTGGCTTCTAGA 49272

QY 1999 ACCAGGCAACTTGGAACTAGACTCCCAAGCTGGAGTATGGCTTACTTTTCAGGCCACAT 2058

Db 49273 ACCAGGCAACTTGGAACTAGACTCCCAAGCTGGAGTATGGCTTACTTTTCAGGCCACAT 49332

QY 2059 GGCTAAAGCAAGTTTCAGAAAGAGTGGGACAGAGCAGAGAACTTTCACCTTCATATATTT 2118

Db 49333 GGCTAAAGCAAGTTTCAGAAAGAGTGGGACAGAGCAGAGAACTTTCACCTTCATATATTT 49392

QY 2119 GTATGATCCTTAATGAATGCATATAAATGTTAAAGTTGATGGTGAATGTAATTAATGTT 2178

Db 49393 GTATGATCCTTAATGAATGCATATAAATGTTAAAGTTGATGGTGAATGTAATTAATGTT 49452

QY 2179 TTTTAACTATGATTTGGAAATTAATCAATGCTATTAATGTTGATAAAG 2232

Db 49453 TTTTAACTATGATTTGGAAATTAATCAATGCTATTAATGTTGATAAAG 49506

RESULT 6
HS095626 143068 bp DNA linear PRI 16-MAY-1997
LOCUS
DEFINITION
Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.

ACCESSION
U95626
VERSION
U95626.1 GI:2104517

KEYWORDS
HTG.
SOURCE
Homo sapiens.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 143068)
McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Nham, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J., Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.

AUTHORS
Human BAC clone 110P12
Unpublished (1997)

TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 143068)
McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Nham, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J., Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.

TITLE
JOURNAL
Direct Submission
Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course, Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor, NY 11724, USA

COMMENT
Regions with single-strand coverage are as follows:

31434 - 31443 37900 - 37968 53303 - 53357
59166 - 59206 63708 - 63998 65200 - 65335
78605 - 78713 92135 - 92137 112377 - 112551
112643 - 112778 134284 - 134309 134914 - 135019
143046 - 144068.

Location/Qualifiers
1. 143068
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="BAC 110P12"
/gene="ccr2"
/note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) mRNA (Accession Number U80924), two alternatively spliced mRNAs."

FEATURES
source

gene

AC098613		AC098613.2		GI:22038607	
AC098613.2		GI:22038607			
HTC.		HTC.			
human.		human.			
Homo sapiens		Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 185437)		1 (bases 1 to 185437)			
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,			
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.			
and Haugen, E.D.		and Haugen, E.D.			
Direct Submission		Direct Submission			
Unpublished		Unpublished			
2 (bases 1 to 185437)		2 (bases 1 to 185437)			
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.			
Direct Submission		Direct Submission			
Submitted (26-OCT-2001) Genome Center, University of Washington,		Submitted (26-OCT-2001) Genome Center, University of Washington,			
Box 352145, Seattle, WA 98195, USA		Box 352145, Seattle, WA 98195, USA			
3 (bases 1 to 185437)		3 (bases 1 to 185437)			
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,			
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.			
and Haugen, E.D.		and Haugen, E.D.			
Direct Submission		Direct Submission			
Submitted (01-AUG-2002) Genome Center, University of Washington,		Submitted (01-AUG-2002) Genome Center, University of Washington,			
Box 352145, Seattle, WA 98195, USA		Box 352145, Seattle, WA 98195, USA			
On Aug 1, 2002 this sequence version replaced gi:16445164.		On Aug 1, 2002 this sequence version replaced gi:16445164.			
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Genome Center		Genome Center			
Center: University of Washington Genome Center		Center: University of Washington Genome Center			
Center Code: UWGC		Center Code: UWGC			
Web site: http://www.genome.washington.edu		Web site: http://www.genome.washington.edu			
Contact: uwgchgs@u.washington.edu		Contact: uwgchgs@u.washington.edu			
-----		-----			
Project Information		Project Information			
-----		-----			
Center project name: chr-3		Center project name: chr-3			
Center clone name: RP11-24F11 (bc0137)		Center clone name: RP11-24F11 (bc0137)			
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Summary Statistics		Summary Statistics			
Sequencing vector: plasmid; L08752; 100% of reads		Sequencing vector: plasmid; L08752; 100% of reads			
Chemistry: Dye-terminator ET; 93% of reads		Chemistry: Dye-terminator ET; 93% of reads			
Assembly: Dye-terminator Big Dye; 7% of reads		Assembly: Dye-terminator Big Dye; 7% of reads			
Consensus quality: 184860 bases at least Q40		Consensus quality: 184860 bases at least Q40			
Consensus quality: 185398 bases at least Q30		Consensus quality: 185398 bases at least Q30			
Consensus quality: 185435 bases at least Q20		Consensus quality: 185435 bases at least Q20			
Insert size: 185437; sum-of-contigs		Insert size: 185437; sum-of-contigs			
Quality coverage: 7.6x in Q20 bases; sum-of-contigs		Quality coverage: 7.6x in Q20 bases; sum-of-contigs			
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Overlapping Sequences:		Overlapping Sequences:			
5': BAC-110P12 U95626, 111014-bp overlap		5': BAC-110P12 U95626, 111014-bp overlap			
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap		3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap			
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Sequence Quality Assessment:		Sequence Quality Assessment:			
This entry has been annotated with sequence quality		This entry has been annotated with sequence quality			
estimates computed by the Phrap assembly program.		estimates computed by the Phrap assembly program.			
All manually edited bases have been reduced to quality zero.		All manually edited bases have been reduced to quality zero.			
Quality levels above 40 are expected to have less than		Quality levels above 40 are expected to have less than			
1 error in 10,000 bp.		1 error in 10,000 bp.			
Base-by-base quality values are not generally visible from the		Base-by-base quality values are not generally visible from the			
Genbank flat file format but are available as part		Genbank flat file format but are available as part			
of this entry's ASN.1 file.		of this entry's ASN.1 file.			
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This sequence was finished as follows unless otherwise noted:		This sequence was finished as follows unless otherwise noted:			
all regions were either double-stranded or sequenced with an		all regions were either double-stranded or sequenced with an			
alternate chemistry or covered by high quality data (i.e., Phred		alternate chemistry or covered by high quality data (i.e., Phred			
quality >= 30); an attempt was made to resolve all sequencing		quality >= 30); an attempt was made to resolve all sequencing			
problems, such as compressions and repeats; all regions were		problems, such as compressions and repeats; all regions were			
covered by at least one plasmid subclone or more than one M13		covered by at least one plasmid subclone or more than one M13			
subclone; and the assembly was confirmed by restriction digest.		subclone; and the assembly was confirmed by restriction digest.			
-----		-----			
Sequence Validation:		Sequence Validation:			
This sequence has been validated by Multiple Complete Digest		This sequence has been validated by Multiple Complete Digest			
fingerprinting. Comparison of the experimentally derived digest		fingerprinting. Comparison of the experimentally derived digest			
fragments with sequence-predicted fragments is given below.		fragments with sequence-predicted fragments is given below.			
The electronically digested sequence consists of both insert and		The electronically digested sequence consists of both insert and			
vector, in order to accurately represent the entire circular BAC.		vector, in order to accurately represent the entire circular BAC.			
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AC098613		AC098613			
AC098613.2		AC098613.2			
GI:22038607		GI:22038607			
HTC.		HTC.			
human.		human.			
Homo sapiens		Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 185437)		1 (bases 1 to 185437)			
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,			
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.			
and Haugen, E.D.		and Haugen, E.D.			
Direct Submission		Direct Submission			
Unpublished		Unpublished			
2 (bases 1 to 185437)		2 (bases 1 to 185437)			
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.			
Direct Submission		Direct Submission			
Submitted (26-OCT-2001) Genome Center, University of Washington,		Submitted (26-OCT-2001) Genome Center, University of Washington,			
Box 352145, Seattle, WA 98195, USA		Box 352145, Seattle, WA 98195, USA			
3 (bases 1 to 185437)		3 (bases 1 to 185437)			
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,			
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.		Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.			
and Haugen, E.D.		and Haugen, E.D.			
Direct Submission		Direct Submission			
Submitted (01-AUG-2002) Genome Center, University of Washington,		Submitted (01-AUG-2002) Genome Center, University of Washington,			
Box 352145, Seattle, WA 98195, USA		Box 352145, Seattle, WA 98195, USA			
On Aug 1, 2002 this sequence version replaced gi:16445164.		On Aug 1, 2002 this sequence version replaced gi:16445164.			
-----		-----			
Genome Center		Genome Center			
Center: University of Washington Genome Center		Center: University of Washington Genome Center			
Center Code: UWGC		Center Code: UWGC			
Web site: http://www.genome.washington.edu		Web site: http://www.genome.washington.edu			
Contact: uwgchgs@u.washington.edu		Contact: uwgchgs@u.washington.edu			
-----		-----			
Project Information		Project Information			
-----		-----			
Center project name: chr-3		Center project name: chr-3			
Center clone name: RP11-24F11 (bc0137)		Center clone name: RP11-24F11 (bc0137)			
-----		-----			
Summary Statistics		Summary Statistics			
Sequencing vector: plasmid; L08752; 100% of reads		Sequencing vector: plasmid; L08752; 100% of reads			
Chemistry: Dye-terminator ET; 93% of reads		Chemistry: Dye-terminator ET; 93% of reads			
Assembly: Dye-terminator Big Dye; 7% of reads		Assembly: Dye-terminator Big Dye; 7% of reads			
Consensus quality: 184860 bases at least Q40		Consensus quality: 184860 bases at least Q40			
Consensus quality: 185398 bases at least Q30		Consensus quality: 185398 bases at least Q30			
Consensus quality: 185435 bases at least Q20		Consensus quality: 185435 bases at least Q20			
Insert size: 185437; sum-of-contigs		Insert size: 185437; sum-of-contigs			
Quality coverage: 7.6x in Q20 bases; sum-of-contigs		Quality coverage: 7.6x in Q20 bases; sum-of-contigs			
-----		-----			
Overlapping Sequences:		Overlapping Sequences:			
5': BAC-110P12 U95626, 111014-bp overlap		5': BAC-110P12 U95626, 111014-bp overlap			
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap		3':			

Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII				EcoRI				HindIII			
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
11786	12040	8696	8837	9531	9423						
2067	2065	6	<800	6382	6501						
5681	5720	1846	1824	512	<800						
3716	3953	4052	3986	449	<800						
875	897	1159	1130	6692	6501						
910	897	54	<800	10449	10229						
2169	2215	560	<800	953	1025						
1705	1653	2287	2267	3124	3176						
5763	5720	4905	4891	1054	1025						
5844	5720	3049	3078	3985	3998						
5061	5001	1377	1394	1100	1025						
2625	2640	9903	9772	124	<800						
725	<800	1022	1021	2671	2693						
1173	1161	12606	12503	1948	1968						
5747	5720	866	868	83	<800						
9995	9684	9817	9772	7455	7474						
999	999	3598	3601	1305	1267						
4541	4503	452	<800	1047	1025						
2950	2981	7549	7635	3299	3301						
406	<800	2063	2075	5279	5237						
3375	3602	5837	5858	6815	6926						
13024	13045	13685	13328	435	<800						
416	<800	4104	3986	2509	2576						
10298	10140	1943	1928	2218	2172						
1478	1452	3964	3986	3797	3802						
287	<800	2758	2771	7758	7830						
205	<800	167	<800	16192	16442						
9428	9684	1307	1304	11020	10820						
3809	3953	13306	13328	1978	1968						
1275	1234	2423	2450	8741	8681						
3351	3381	2243	2267	4795	4815						

FEATURES		Location/Qualifiers	
source		1..185437	
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		/chromosome="3"	
		/clone="RP11-24F11"	
Query Match		49.3%; Score 1101; DB 9; Length 185437;	
Best Local Similarity		99.8%; Pred. No. 0;	
Matches 1251; Conservative		0; Mismatches 3; Indels 0; Gaps 0;	
QY	979	AGCCTTTTTCACATAGCTCTGGCTGTAGGATGCCACCTCCAAACCAAGTGTGGA	1038
Db	16204	AGCCTTTTTCACATAGCTCTGGCTGTAGGATGCCACCTCCAAACCAAGTGTGGA	16263
QY	1039	GGTCCAGGAGTGACAGCAAGAAAGTGTGAAAGTGACTACACAGGACTCTCGATGGT	1098
Db	16264	GGTCCAGGAGTGACAGCAAGAAAGTGTGAAAGTGACTACACAGGACTCTCGATGGT	16323
QY	1099	CGTGGAAAGGAAGTCAATTGGCAGAGCCCTGAAGCCAGTCTTCAGGACAAAGGA	1158
Db	16324	CGTGGAAAGGAAGTCAATTGGCAGAGCCCTGAAGCCAGTCTTCAGGACAAAGGA	16383
QY	1159	GCTAGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTTTCACAGATG	1218
Db	16384	GCCTAGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTTTCACAGATG	16443

[illegible]

G07239
G07239.1 GI:860484
STS; STS sequence; primer; sequence tagged site.
Homo sapiens STSs derived from sequences in dbEST and the Unigene
collection.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
Hudson, T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)

Contact: Thomas Hudson
 Whitehead Institute/MIT Center for Genome Research
 Whitehead Institute for Biomedical Research
 9 Cambridge Center, Cambridge MA 02142 USA
 Tel: 617 252 1900
 Fax: 617 252 1902
 Email: thudson@genome.wi.mit.edu

Primer A: GGAAATCACACGTCTGGCTT
Primer B: ACTGTTTTCCAACCCAGCTG
STS size: 114
PCR Profile:

presoak:
 Denaturation:
 Annealing: 56 degrees C
 Polymerization:
 PCR Cycles: 35
 Thermal Cycler:

Protocol:

- Template: 10 ng
- Primer: each 5 pM
- dNTPs: each 4 nM
- Taq Polymerase: 0.025 units/ul
- Total Vol: 20 ul

Buffer:
MgCl₂: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

prepared with primer pairs derived from U03882 -- Unigene.

FEATURES source

1. .1068
/organism="Homo sapiens"
/Ab xref="taxon.9606"

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/db_xref="taxon:9606"  
/map="730_D_5; 913_C_5; 941_A_7; 743_H_10; 781_B_10;  
881_F_10; 881_F_11"
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STS
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  primer_bind 27..46
  primer_bind complement(121..140)
  primer_bind 186..238
  primer_bind 315..329

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Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	1165	AGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCTGGCTTCACAGATGTGTGAT	1224
DB	1	AGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCTGGCTTCACAGATGTGTGAT	60
QY	1225	TCACAGTGTGAATCTTGGTGTCTACGTTACCCAGCAGGAAGGCTGAGAGGAGAGAGACTC	1284
DB	1	TCACAGTGTGAATCTTGGTGTCTACGTTACCCAGCAGGAAGGCTGAGAGGAGAGAGACTC	120

Qy 1285 CAGCTGGGTTGGAAAAAGAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTGAATACA 1344
|||||
pb 121 CAGCTGGGTTGGAAAAAGAGTATTTTCCAAACTACCTTCCAGTTCCTCATTTTGAATACA 180

RESULT 8			
G07239			
LOCUS	G07239	1068 bp	DNA
DEFINITION	human STS WI-9314, sequence tagged site.		linear
			STS 19-OCT-1995

QY 1345 GCATAGAGTTCAGACTTTTAAATAGTAAATAAATAAAGCTGAAAGTGCAC 1404
Db 181 GCATAGAGTTCAGACTTTTAAATAGTAAATAAATAAAGCTGAAAGTGCAC 240
QY 1405 TTGTAATCTGGTAAAGAGTGTAGTTGAGTTCATATGTCACAAAGCTGAAATGCTGA 1464
Db 241 TTGTAATCTGGTAAAGAGTGTAGTTGAGTTCATATGTCACAAAGCTGAAATGCTGA 300
QY 1465 TTAGTCACAGAGATAATTTAGCTTTGAGCTTAAGAAATTTGAGCAGCTGTATGTTGG 1524
Db 301 TTAGTCACAGAGATAATTTAGCTTTGAGCTTAAGAAATTTGAGCAGCTGTATGTTGG 360
QY 1525 GAGACTGCTGAGTCAACCCCAATAGTTGTTGATTTGGCAGGAGTTGGAAGTGTGATCTGT 1584
Db 361 GAGACTGCTGAGTCAACCCCAATAGTTGTTGATTTGGCAGGAGTTGGAAGTGTGATCTGT 420
QY 1585 GGGCACATTAAGCCATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1644
Db 421 GGGCACATTAAGCCATGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 1645 ACCTCCATGCTGTCATGTCAGTGTGATGTCATGTCATGTCATGTCATGTCATGTCAT 1704
Db 481 ACCTCCATGCTGTCATGTCAGTGTGATGTCATGTCATGTCATGTCATGTCATGTCAT 540
QY 1705 TTTTGTGTTTGTGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1764
Db 541 TTTTGTGTTTGTGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 1765 GTGCTTCGCGAGTGTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1824
Db 601 GTGCTTCGCGAGTGTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 1825 AATCAAAATGGCTTCTAATCAAAAGCTTTAAACCCATTGGTAAAGAAATGGAAGTGGAG 1884
Db 661 AATCAAAATGGCTTCTAATCAAAAGCTTTAAACCCATTGGTAAAGAAATGGAAGTGGAG 720
QY 1885 AAGTCCCTGAAGTAAAGAAAGCTTTTCTTCTAGTGCAGCCAAAGTAAAGATGTTCTTA 1944
Db 721 AAGTCCCTGAAGTAAAGAAAGCTTTTCTTCTAGTGCAGCCAAAGTAAAGATGTTCTTA 780
QY 1945 TGTGCGCAGTGTGTTTCTGATCTGATGCAAGCAAGAAACACTGGGCTTCTAGAACCCAGG 2004
Db 781 TGTGCGCAGTGTGTTTCTGATCTGATGCAAGCAAGAAACACTGGGCTTCTAGAACCCAGG 840
QY 2005 CAACCTGGGAAGTACAGTCCCAAGCTGGAGTATGCTTCTAGTGCAGCCAAAGTAA 2064
Db 841 CAACCTGGGAAGTACAGTCCCAAGCTGGAGTATGCTTCTAGTGCAGCCAAAGTAA 900
QY 2065 AGAAGGTTTCAGAAAGAGTGGGACAGACAGAGAACTTTCACCTTCATATATTTGATGA 2124
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QY 2125 TCCTAATGAATGCATAAATGTTAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2184
Db 961 TCCTAATGAATGCATAAATGTTAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 2185 AACTATGATTTGAAAATAAATCAATGCTATAAATGCTATGCTGATGATGATGATGAT 2232
Db 1021 AACTATGATTTGAAAATAAATCAATGCTATAAATGCTATGCTGATGATGATGATGAT 1068

RESULT 9
ARL16075
LOCUS
DEFINITION Sequence 3 from patent US 6132987.
ACCESSION ARL16075
VERSION ARL16075.1 GI:14096397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1979)
PAT 16-MAY-2001

AUTHORS Charo, I.F. and Coughlin, S.R.
TITLE Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)
JOURNAL Patent: US 6132987-A 3 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..1979
BASE COUNT 530 a 435 c 451 g 563 t
ORIGIN /organism="unknown"

Query Match 43.9%; Score 980; DB 6; Length 1979;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGAACAAGGAGCGCATTTCCCGAGTACATCCACAACATGCTGTCACACATCTGTTCT 60
Db 42 GGATGAACAAGGAGCGCATTTCCCGAGTACATCCACAACATGCTGTCACACATCTGTTCT 101
QY 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCAACACCTTTTGGATTATGAT 120
Db 102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCAACACCTTTTGGATTATGAT 161
QY 121 TACGGTCTCCCTGTCATATAATTTGACGTGAAGCAAAATTTGGGGCCCAACTCCTGCCCTCG 180
Db 162 TACGGTCTCCCTGTCATATAATTTGACGTGAAGCAAAATTTGGGGCCCAACTCCTGCCCTCG 221
QY 181 CTCTACTCGCTGGTGTTCATCTTTGGTGTGGGCAACATGCTGTCGTCCTCATCTTA 240
Db 222 CTCTACTCGCTGGTGTTCATCTTTGGTGTGGGCAACATGCTGTCGTCCTCATCTTA 281
QY 241 ATAACTGCAAAAAGCTGAAGTCTTCACTGACATTTACCTGTCACACCTGGCCATCTCT 300
Db 282 ATAACTGCAAAAAGCTGAAGTCTTCACTGACATTTACCTGTCACACCTGGCCATCTCT 341
QY 301 GATCTCTTTTCTTATTAATCTCCCATTTGGGCTCACTCTGCTCAAAATGAGTGGGTC 360
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QY 361 TTGGGAATGCATGTGCAAAATTTTCAAGGGCTGTATCACATCGGTTATTTTGGCGGA 420
Db 402 TTGGGAATGCATGTGCAAAATTTTCAAGGGCTGTATCACATCGGTTATTTTGGCGGA 461
QY 421 ATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGGCTATTCCTGCTGCTGTTT 480
Db 462 ATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGGCTATTCCTGCTGCTGTTT 521
QY 481 GCTTTAAAGCCAGGACGGTCACTTTGGGCTGTGACAAGTGTGATCATCACCTGGTGGTG 540
Db 522 GCTTTAAAGCCAGGACGGTCACTTTGGGCTGTGACAAGTGTGATCATCACCTGGTGGTG 581
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Db 1002 GTTGGGAGAGTTCAGAG 1021
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RESULT 10
LOCUS I79543 179543 1979 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 3 from patent US 5707815.
ACCESSION I79543
VERSION I79543.1 GI:3207833
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1979)
AUTHORS Charo,I.F. and Coughlin,S.R.
TITLE Mammalian monocyte chemoattractant protein receptors and assays using them
JOURNAL Patent: US 5707815-A 3 13-JAN-1998;
FEATURES Location/Qualifiers
source 1. 1979
BASE COUNT 530 a 435 c 451 g 563 t
ORIGIN
Query Match 43.9%; Score 980; DB 6; Length 1979;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGATTGAACAAGAGCGATTTCCCGAGTACATCCCAACATGCTGTCCACATCTCGTTCT 60
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Db 582 GCTGTGTTTGTCTGTGCCAGGAATCATCTTTACTAAATGCCAGAAAGATTCTGTT 641
QY 601 TATGTCGTGGCCCTTATTTTCCAGGAGATGGAAATATTTCCACACAATATGAGGAAC 660
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Db 942 CAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCTTTC 1001
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Db 1002 GTTGGGAGAGTTCAGAG 1021
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RESULT 11
LOCUS HSU03905 1979 bp mRNA linear PRI 22-JUN-1994
DEFINITION Human monocyte chemoattractant protein 1 receptor (MCP-1RB) alternatively spliced mRNA, complete cds.
ACCESSION U03905
VERSION U03905.1 GI:472557
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1979)
AUTHORS Charo,I.F., Myers,S.J., Herman,A., Franci,C., Connolly,A.J. and Coughlin,S.R.
TITLE Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)
MEDLINE 94195821
PUBMED 8146186
REFERENCE 2 (bases 1 to 1979)
AUTHORS Myers,S.J.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110, USA
FEATURES Location/Qualifiers
source 1. 1979
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cor2-2a"
/cell_line="MonoMac 6"
/clone_lib="MM6-#3"
81.1163
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/note="alternatively spliced; MCP-1RB"
/codon_start=1
/product="MCP-1 receptor"
/protein_id="AAA19120.1"
/db_xref="GI:472558"

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VICYSGILKLLRCRNEKKHRAVRVIFTIMVYFLEWYINIVILLNTQEEFGLSN
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FYRETVDGVSTINTPSTGEQEVASGL"
BASE COUNT 530 a 435 c 451 g 563 t
ORIGIN

Query Match 43.9%; Score 980; DB 9; Length 1979;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATTGAACAGGAGCGATTCCCGAGTACATCCACAAATGCTGTCCACATCCGTTCT 60
DB 42 GGATTGAACAGGAGCGATTCCCGAGTACATCCACAAATGCTGTCCACATCCGTTCT 101
QY 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGTCAACACCTTTTGTGATTATGAT 120
DB 102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGTCAACACCTTTTGTGATTATGAT 161
QY 121 TAGGTCCTCCCTGTCTAATAATTTGAGTGAAGCAAAATGGGGCCCAACCTCCCTCCG 180
DB 162 TAGGTCCTCCCTGTCTAATAATTTGAGTGAAGCAAAATGGGGCCCAACCTCCCTCCG 221
QY 181 CTCTACTCGCTGGTGTCTATCTTTGGTTTGGGCAACATGCTGCTCCTCATCTTA 240
DB 222 CTCTACTCGCTGGTGTCTATCTTTGGTTTGGGCAACATGCTGCTCCTCATCTTA 281
QY 241 ATAACTGCAAAAGCTGAAGTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 282 ATAACTGCAAAAGCTGAAGTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 341
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DB 342 GATCTGCTTTTCTTATTTACTTCCCATTTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 401
QY 361 TTGGGAATGCAATGTGCAAAATTTTACAGGCTGTATACATCGGTTATTTTGGCGGA 420
DB 402 TTGGGAATGCAATGTGCAAAATTTTACAGGCTGTATACATCGGTTATTTTGGCGGA 461
QY 421 ATCTTCTTCATCATCTCTGCAATGATATACCTGGCTTATGCTCATGCTGCTGTT 480
DB 462 ATCTTCTTCATCATCTCTGCAATGATATACCTGGCTTATGCTCATGCTGCTGTT 521
QY 481 GCTTTAAAGCCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 522 GCTTTAAAGCCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
QY 541 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 582 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
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ACCESSION AX232508
VERSION AX232508.1 GI:15592570
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REFERENCE 1 (bases 1 to 1083)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Valdes, A.M., Groot, P.H. and Spurr, N.K.
JOURNAL Cr2-64i, polymorphic variant of the human cor2 receptor and its
use in the diagnostic and treatment of atherosclerosis
PATENT: WO 0162796-A 30-AUG-2001;
SMITHKLINE BEECHAM PLC (GB)
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Query Match 42.2%; Score 941; DB 6; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 100 ACCACCTTTTGTGATTATGATTACGCTGCTCCCTGTGCATAAATTTACCTGGAAGCAAT 159
DB 61 ACCACCTTTTGTGATTATGATTACGCTGCTCCCTGTGCATAAATTTACCTGGAAGCAAT 120
QY 160 GGGCCCCAAGCTCCTGCTCCGCTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219
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REFERENCE			
AUTHORS			
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REFERENCE			

AUTHORS
TITLE
JOURNAL

COMMENT

Yamagami, S.
Direct Submission
Submitted (22-APR-1994) Shinsuke Yamagami, TEIJIN LIMITED,
Institute for Bio-Medical Research; 4-3-2 Asahigaoka, Hino, Tokyo
191, Japan (Tel:0425-86-8282)
Submitted (22-Apr-1994) to DBJ by:
Shinsuke Yamagami
Teijin Limited
Institute for Bio-Medical Research
4-3-2 Asahigaoka
Hino, Tokyo 191
Japan
Phone: 0425-86-8282
Fax: 0425-87-5512

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5

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Db	541	TGCCAGAAAAGAGATTCTGTTTATGCTGTGGCCCTTATTTTCCAGGAGATGGAATAAT	600
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QY	760	GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTCTCTCTGGACTCCCTATAAT	819
Db	721	GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTCTCTCTGGACTCCCTATAAT	780
QY	820	ATTGTGATTCCTCGAACACCTTCAGAAATTCCTTCGGCCTGAGTAACTGTGAAAGCACC	879
Db	781	ATTGTGATTCCTCGAACACCTTCAGAAATTCCTTCGGCCTGAGTAACTGTGAAAGCACC	840
QY	880	AGTCACTGGACCAAGCCACGACGAGTGCACAGACTCTTGGGAGAGTTCAGAAG	939
Db	841	AGTCACTGGACCAAGCCACGACGAGTGCACAGACTCTTGGGAGAGTTCAGAAG	900
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AX280849

LOCUS

DEFINITION

AX280849

Sequence 472 from Patent 5,911,120

1083 bp

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PAT 02-NOV-2001

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source
BASE COUNT
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Mon Jun' 2 09:42:04 2003

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